Respectfully submitted,

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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification

Paragraph beginning at page 1 after the title has been amended as follows:

Cross Reference to Related Application

This application claims benefit of U.S. Provisional Application Serial No. 60/243,913, filed October 27, 2000, which application is incorporated herein by reference.

Paragraph beginning at line 21, page 6, has been amended as follows:

Figure 7 shows an amino acid sequence of recombinant human TPO (SEQ ID NO:13).

Paragraph beginning at line 17, page 19, has been amended as follows:

An immunodominant epitope of human thrombopoietin includes amino acids 318 to 332 and has the following sequence (represented in single letter code):

LNTSYTHSQNLSEQ (SEQ ID NO:1)

Paragraph beginning at line 7, page 22, has been amended as follows:

Analysis of the amino acid sequence of human thrombopoietin resulted in the identification of a predicted immunodominant epitope using the service provided by Epivax, Inc. Fourteen out of 15 amino acid residues of the immunodominant peptide identified using antibodies from naïve patients showed 100% homology with the 14 residues at the C-terminal of the 20 amino acid region predicted by EpiVax. The sequence of the predicted immunodominant epitope has an amino acid sequence identical to amino acid residues 312 to 331:

TPTSPLLNTSYTHSQNLSQE (SEQ ID NO: 2)

Paragraph beginning at line 8, page 40, has been amended as follows:

A specific example of a modified polypeptide is a modified thrombopoietin having reduced immunogenicity while retaining substantial therapeutic activity. An

immunodominant epitope in native sequence human thrombopoietin is a c-terminal peptide including amino acids 318 to 332 :

LNTSYTHSQNLSQEG (SEQ ID NO.: 1)

The table beginning at line 14, page 50, with the following rewritten paragraph:

Table 2

Synthetic TPO c-terminal epitope peptides

and corresponding rabbit anti-peptide antibodies

peptide sequence (length)	antibody ID #
154-170(17)	24
175-190(16)	48
195-211(17)	28
18-234(17)	19
244-259(16)	17
258-268(11)	49
268-283(16)	16
296-311(16)	51
318-332(15)	15

The peptides have the following sequences:

154- 170	RAPPTTAVPSRTSLVLT (SEQ ID NO: 3)
175-190	PNRTSGLLETNFTASA (SEQ ID NO: 4)
195-211	SGLLKWQQGFRAKIPGL (SEQ ID NO: 5)
218-234	SLDQIPGYLNRIHELLN (SEQ ID NO: 6)
244-259	SRRTLGAPDISSGTSD (SEQ ID NO: 7)
258-268	SDTGSLPPNLQ (SEQ ID NO: 8)

268-283 QPGYSPSPTHPPTGQY (SEQ ID NO: 9)

296-311 VVQLHPLLPDPSAPTP (SEQ ID NO: 10)

318-332 LNTSYTHSQNLSQEG (SEQ ID NO: 1)

Paragraph beginning at line 12, page 52, has been amended as follows:

The entire linear amino acid sequence of human recombinant TPO was provided to EpiVax, Inc. for analysis and prediction of immunodominant epitopes. The results from EpiVax, Inc. identified 3 regions within the c-terminal epitope that have class II MHC binding motifs. One of these predicted epitope regions (identical to amino acids 312-331) is shown:

TPTSPLLNTSYTHSQNLSQE (SEQ ID NO: 2)

Paragraph beginning at line 17, page 53, has been amended as follows:

A cDNA corresponding to the hTPO entire open reading frame was obtained by PCR using the oligonucleotide primes of the following Table.

CHO Expression Vector PCR Primers

Cla.FL.F2 5' ATC GAT ATC GAT AGC CAG ACA CCC CGG CCA G 3' (SEQ ID NO:11)
ORF.Sal 5' AGT CGA CGT CGA CGT CGG CAG TGT CTG AGA ACC 3' (SEQ ID NO:12)

PRK5-*hmpl* I was used as template for the reaction in the presence of pfu DNA polymerase (Stratagene). Initial denaturation was for 7 min. at 94°C followed by 25 cycles of amplification (1 min. at 94°C, 1 min. at 55°C and 1 min. at 72°C). Final extension was for 15 min. at 72°C. The PCR product was purified and cloned between the restriction sites ClaI and SalI of the plasmid pSV15.ID.LL to obtain the vector pSV15.ID.LL.MLORF.The sequence of the construct was verified.